Amendment to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A method for comparing gene expression level~~,~~ comprising the following steps ~~characterized in that the method~~ includes:
(a) labeling mRNA from different sources with ~~a suitable method~~DNA fragments having different base orders, and mixing the labeled ~~mRNA fragments~~ molecules equally to obtain a template for polymerase chain reaction (PCR);
(b) performing a polymerase chain reaction using source-specific primers with different sequences and ~~a~~ gene-specific primers; and
(c) quantitatively detecting a sequence of amplified DNA ~~fragments~~ mixture ~~with~~ by bioluminescence analysis, preferably pyrosequencing, ~~a~~ the base type ~~and a signal intensity~~ in ~~a~~ the sequencing profile, the signal intensity of the corresponding base representing ~~a~~ the gene source and a relative expression level at the source~~, respectively~~.

2. (original) The method for comparing gene expression level according to claim 1, wherein the mRNA from different sources is an expressed mRNA of a given gene from different individuals of a species, or is an expressed mRNA of a given gene from different organs of an individual, or is an expressed mRNA of a given gene of a same species at different states of chemical stimulation or physical stimulation.

3. (currently amended) The method for comparing gene expression level according to claim 1, wherein each of the source-specific primers includes an identical base species and base number but a different base order, each primer representing a gene source.

4. (currently amended) The method for comparing gene expression level according to claim 1, wherein ~~the suitable method is a method to distinguish a gene source by a DNA fragment with a suitable length,~~ labeling mRNA from different sources with DNA fragments having different base order includes three methods for the labeling:

a first of the method including:

performing a reverse transcription-polymerase chain reaction (RT -PCR) to obtain complementary DNA(cDNA) fragments of a given gene in each source;

digesting cDNA into fragments with a suitable length using a restriction endonuclease; and

ligating each of the digested cDNA fragments with a selective adapter, a different adapter corresponding to mRNA from a different source; or

a second of the method including:

synthesizing a first strand of complementary DNA (cDNA) fragments of mRNA samples from each source using polythymine primers fixed on microsphere's surface; and

synthesizing a complementary second strand of cDNA using anchored primers containing sequences corresponding to gene sources in a 5'-terminal region, a 5'-terminal region being used for identifying different sources of a given gene; or

~~and~~ a third of the method including:

preparing a first strand of the complementary DNA(cDNA) fragments of mRNA samples from each source by directly

hybridizing anchored primers containing sequences corresponding to gene sources in a 5'-terminal region with mRNA; and constructing of a 5'-terminal region of the anchored primers the same as that in the second of the method.

5. (currently amended) The method for comparing gene expression level according to claim 4, wherein the selective adapter is a cuneal dsDNA (double strand DNA) containing a part of sequences complementary to recognition sequences of the restriction endonuclease and can be fully ligated with restriction enzyme cutting ends in DNA fragment by a DNA ligase, a 5' terminal region of one of the strands in the adapter containing ~~a sequence specific to gene sources~~an arbitrary sequence, used to represent the particular gene source it's ligating to, a 3'terminal region of the other strand in the adapter containing bases non-complementary to a opposite strand, or a 3' end of the other strand in the adapter being modified to block ability of extension reaction by DNA polymerase, and the adapter having a structure of a "Y" shape consisting of two strands, one end of the adapter being divided into two branches due to no complementary bases, and the other end being formed of a shape of restriction enzyme cutting site.

6. (currently amended) The method for comparing gene expression level according to claim ~~4~~1 claim 4, wherein the ~~part used for identifying gene sources in selective adapters and anchored primers~~ DNA fragments includes identical base species and base number but different base order, each of the ~~selective adapters~~ fragments having a same melting temperature~~, and each of the anchored primers including a same melting temperature~~.

7. (original) The method for comparing gene expression level according to claim 1, wherein the bioluminometric assay is based on a quantitative determination of pyrophosphate released from an extension reaction.

8. (currently amended) The method for comparing gene expression level according to claim 7, wherein the extension reaction is polymerization of single-stranded PCR products annealed with a given primer or primer mixtures by DNA polymerase when a deoxynucleotide (dNTP) added in a given order, or a ~~dideoxynecleoide~~ dideoxynucleotide (ddNTP) added in a given order, or an analog of dNTP or ddNTP added in a given order is complementary to the template.

9. (original) The method for comparing gene expression level according to claim 8, wherein the single-stranded PCR products are obtained by treating the PCR products of claim 1 with a physical method or a chemical method, the physical method being to use a biotinylated primer for PCR amplification and then to prepare single-stranded DNAs by a solid phase method, and the chemical method being to use an enzyme for the digestion to prepare single-stranded DNAs.

10. (currently amended) The method for comparing gene expression level according to claim 7, wherein the extension reaction is polymerization of the PCR products ~~of claim 1~~ treated by enzymes to degrade PPi produced during PCR reaction, excess dNTPs and excess primers, a single-strand binding protein (e.g. SSB) being added into the treated PCR products~~, the rest being performed in accordance with claim 8~~.

11. (new) The method for comparing gene expression level according to claim 1, wherein labeling mRNA from different sources with DNA fragments having different base orders includes labeling mRNA from six kinds of sources with DNA fragments having six kinds of different base orders.

12. (new) The method for comparing gene expression level according to claim 11, wherein the six kinds of different base orders include “cgat”, “gcat”, “agct”, “gact”, “cagt” and “acgt”,only three kinds of dNTPs, including dTTP, dGTP, and dCTP, are used in the bioluminescence analysis.